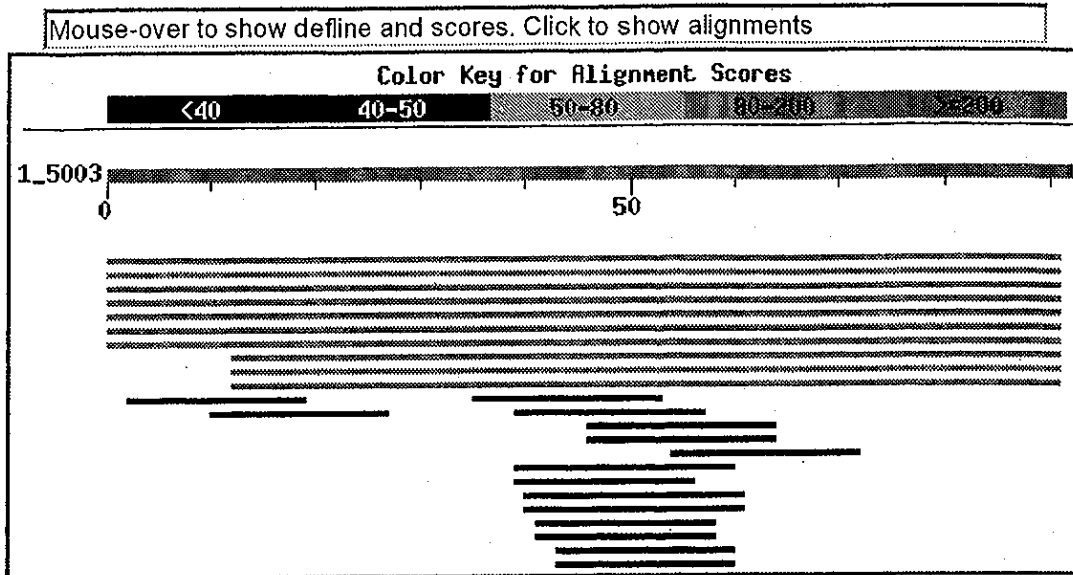


Part of the  
office action

Attachment for sequencing search

**Distribution of 25 Blast Hits on the Query Sequence**



Sequences producing significant alignments:

Score E  
(bits) Value

<a href="#">gi 24054235 gb AE015383.1 </a>	Shigella flexneri 2a str. 301 se...	<u>182</u>	6e-44
<a href="#">gi 30043176 gb AE016991.1 </a>	Shigella flexneri 2a str. 2457T ...	<u>182</u>	6e-44

gi 2367266 gb AE000447.1 AE000447	Escherichia coli K12 MG16...	182	6e-44
gi 290484 gb L10328.1 ECOUW82	E. coli; the region from 81.5...	182	6e-44
gi 12518536 gb AE005601.1 AE005601	Escherichia coli O157:H7...	174	1e-41
gi 13363930 dbj AP002566.1	Escherichia coli O157:H7 DNA, c...	174	1e-41
gi 26110701 gb AE016769.1	Escherichia coli CFT073 section ...	167	4e-39
gi 29139451 gb AE016846.1	Salmonella enterica subsp. enter...	111	2e-22
gi 16504729 emb AL627280.1	Salmonella enterica serovar Typ...	111	2e-22
gi 16422410 gb AE008879.1	Salmonella typhimurium LT2, sect...	103	5e-20
gi 14589682 gb AC020589.4	Homo sapiens BAC clone RP11-143G...	38	2.2
gi 24202118 gb AE011592.1	Leptospira interrogans serovar l...	38	2.2
gi 17739388 gb AE009065.1 AE009065	Agrobacterium tumefacien...	38	2.2
gi 15156031 gb AE008032.1 AE008032	Agrobacterium tumefacien...	38	2.2
gi 14193024 gb AC013718.6	Homo sapiens BAC clone RP11-116I...	38	2.2
gi 19909496 gb AC098742.4	Mus musculus BAC clone RP23-122N...	36	8.8
gi 33147141 gb AC144644.3	Medicago truncatula clone mth2-1...	36	8.8
gi 18642908 gb AC080132.6	Homo sapiens BAC clone RP11-166B...	36	8.8
gi 29243387 dbj AP001011.6	Homo sapiens genomic DNA, chrom...	36	8.8
gi 29243373 dbj AP005061.3	Homo sapiens genomic DNA, chrom...	36	8.8
gi 13810526 dbj AP000923.5	Homo sapiens genomic DNA, chrom...	36	8.8
gi 15787722 emb AL162574.14	Human DNA sequence from clone ...	36	8.8
gi 16944202 emb AL603792.12	Mouse DNA sequence from clone ...	36	8.8
gi 15128594 dbj AB055625.1	Inversidens japonensis mitochon...	36	8.8
gi 14043054 emb AL450324.10	Human DNA sequence from clone ...	36	8.8

#### Alignments

Get selected sequences

Select all

Deselect all

☐ >gi|24054235|gb|AE015383.1| ☒ Shigella flexneri 2a str. 301 section 346 of 412 o  
genome  
Length = 10768

Score = 182 bits (92), Expect = 6e-44  
Identities = 92/92 (100%)  
Strand = Plus / Plus

Query: 1 gaagagatgttcagggttttcggttatcggaatggtatcgaaacttgatatttctcatacttc 60  
|||||  
Sbjct: 2512 gaagagatgttcagggttttcggttatcggaatggtatcgaaacttgatatttctcatacttc 2571

Query: 61 tcgtcaggcgtggagtagcgcgcgccacggaa 92  
|||||  
Sbjct: 2572 tcgtcaggcgtggagtagcgcgcgccacggaa 2603

☐ >gi|30043176|gb|AE016991.1| ☒ Shigella flexneri 2a str. 2457T section 14 of 16 o  
Length = 293558

Score = 182 bits (92), Expect = 6e-44  
Identities = 92/92 (100%)  
Strand = Plus / Minus

Query: 1 gaagagatgttcagggttttcggttatcggaatggatcgaaacttgatatttctcatacttc 60  
|||||  
Sbjct: 117498 gaagagatgttcagggttttcggttatcggaatggatcgaaacttgatatttctcatacttc 117439


Query: 61 tcgtcaggcgtggagtagccgcgccacggaa 92  
|||||  
Sbjct: 117438 tcgtcaggcgtggagtagccgcgccacggaa 117407

☐ >gi|2367266|gb|AE000447.1|AE000447  Escherichia coli K12 MG1655 section 337 of  
Length = 11355

Score = 182 bits (92), Expect = 6e-44  
Identities = 92/92 (100%)  
Strand = Plus / Minus

Query: 1 gaagagatgttcagggttttcggttatcggaatggatcgaaacttgatatttctcatacttc 60  
|||||  
Sbjct: 8832 gaagagatgttcagggttttcggttatcggaatggatcgaaacttgatatttctcatacttc 8773


Query: 61 tcgtcaggcgtggagtagccgcgccacggaa 92  
|||||  
Sbjct: 8772 tcgtcaggcgtggagtagccgcgccacggaa 8741

☐ >gi|290484|gb|L10328.1|ECOUW82  E. coli; the region from 81.5 to 84.5 minutes  
Length = 136254

Score = 182 bits (92), Expect = 6e-44  
Identities = 92/92 (100%)  
Strand = Plus / Minus

Query: 1 gaagagatgttcagggttttcggttatcggaatggatcgaaacttgatatttctcatacttc 60  
|||||  
Sbjct: 75216 gaagagatgttcagggttttcggttatcggaatggatcgaaacttgatatttctcatacttc 75157

Query: 61 tcgtcaggcgtggagtagccgcgccacggaa 92  
|||||  
Sbjct: 75156 tcgtcaggcgtggagtagccgcgccacggaa 75125

☐ >gi|12518536|gb|AE005601.1|AE005601  Escherichia coli O157:H7 EDL933 genome, co  
290  
Length = 11316

Score = 174 bits (88), Expect = 1e-41  
Identities = 91/92 (98%)  
Strand = Plus / Minus

Query: 1 gaagagatgttcagggttttcggttatcggaatggatcgaaacttgatatttctcatacttc 60

|||||  
Sbjct: 8839 gaagagatgttcagggttttcggtatcggcaatggtatcgaacttgatatttctcgtaacttc 8780

Query: 61 tcgtcaggcgtggagtagcgcgcgccacggaa 92  
|||||  
Sbjct: 8779 tcgtcaggcgtggagtagcgcgcgccacggaa 8748

☐ >gi|13363930|dbj|AP002566.1| ☒ Escherichia coli O157:H7 DNA, complete genome, se  
Length = 280900

Score = 174 bits (88), Expect = 1e-41  
Identities = 91/92 (98%)  
Strand = Plus / Minus

Query: 1 gaagagatgttcagggttttcggtatcggcaatggtatcgaacttgatatttctcataacttc 60  
|||||  
Sbjct: 185002 gaagagatgttcagggttttcggtatcggcaatggtatcgaacttgatatttctcgtaacttc 184943

Query: 61 tcgtcaggcgtggagtagcgcgcgccacggaa 92  
|||||  
Sbjct: 184942 tcgtcaggcgtggagtagcgcgcgccacggaa 184911

☐ >gi|26110701|gb|AE016769.1| ☒ Escherichia coli CFT073 section 15 of 18 of the co  
Length = 301566

Score = 167 bits (84), Expect = 4e-39  
Identities = 90/92 (97%)  
Strand = Plus / Minus

Query: 1 gaagagatgttcagggttttcggtatcggcaatggtatcgaacttgatatttctcataacttc 60  
|||||  
Sbjct: 155271 gaagagatgttcagggttttcggtatcggcaatggtatcgaacttgatatttctcgtaacttc 155212

Query: 61 tcgtcaggcgtggagtagcgcgcgccacggaa 92  
|||||  
Sbjct: 155211 tcgtcaggcgtggagtagcgcgcaccacggaa 155180

☐ >gi|29139451|gb|AE016846.1| ☒ Salmonella enterica subsp. enterica serovar Typhi  
of the complete genome  
Length = 300592

Score = 111 bits (56), Expect = 2e-22  
Identities = 74/80 (92%)  
Strand = Plus / Plus


Query: 13 aggttttcggtatcggcaatggtatcgaacttgatatttctcataacttctcgtcaggcgtg 72  
|||||

Sbjct: 181893 aggttttcggttatcggcaatggtgtcgaatttgattttctcatacttctcatccggcggtg 181952

Query: 73 gagtacgccgcgccacggaa 92

||||||| ||||| |||||

Sbjct: 181953 gagtacgctgcgccgcggaa 181972

□ >gi|16504729|emb|AL627280.1|  Salmonella enterica serovar Typhi (Salmonella typ  
complete chromosome; segment 16/20  
Length = 245050

Score = 111 bits (56), Expect = 2e-22

Identities = 74/80 (92%)

Strand = Plus / Plus

Query: 13 aggttttcggttatcggcaatggtatcgaacttgattttctcatacttctcgtcaggcggtg 72


||||||| ||||||| ||||| ||||||| ||||||| || |||||

Sbjct: 74996 aggttttcggttatcggcaatggtgtcgaatttgattttctcatacttctcatccggcggtg 75055

Query: 73 gagtacgccgcgccacggaa 92

||||||| ||||| |||||

Sbjct: 75056 gagtacgctgcgccgcggaa 75075

□ >gi|16422410|qb|AE008879.1|  Salmonella typhimurium LT2, section 183 of 220 of  
Length = 21130

Score = 103 bits (52), Expect = 5e-20

Identities = 73/80 (91%)

Strand = Plus / Minus

Query: 13 aggttttcggttatcggcaatggtatcgaacttgattttctcatacttctcgtcaggcggtg 72


||||||| ||||||| ||||| ||||||| ||||||| || |||||

Sbjct: 4731 aggttttcggttatcggcaatagtgtcgaatttgattttctcatacttctcatccggcggtg 4672

Query: 73 gagtacgccgcgccacggaa 92

||||||| ||||| |||||

Sbjct: 4671 gagtacgctgcgccgcggaa 4652

□ >gi|14589682|gb|AC020589.4|  Homo sapiens BAC clone RP11-143G24 from 4, complet  
Length = 147185

Score = 38.2 bits (19), Expect = 2.2


Identities = 19/19 (100%)

Strand = Plus / Plus

Query: 40 aacttgattttctcatact 58


||||||| |||||||

Sbjct: 37798 aacttgattttctcatact 37816

☐ >[gi|24202118|gb|AE011592.1|](#)  *Leptospira interrogans* serovar lai str. 56601 chro  
4 of 34 of the complete sequence  
Length = 10029


Score = 38.2 bits (19), Expect = 2.2  
Identities = 19/19 (100%)  
Strand = Plus / Plus

Query: 36 atcgaacttgatatttctca 54  
|||||  
Sbjct: 1975 atcgaacttgatatttctca 1993

☐ >[gi|17739388|gb|AE009065.1|AE009065](#)  *Agrobacterium tumefaciens* strain C58 circu  
256 of the complete sequence  
Length = 11490


Score = 38.2 bits (19), Expect = 2.2  
Identities = 19/19 (100%)  
Strand = Plus / Plus

Query: 47 atttctcatacttctcgtc 65  
|||||  
Sbjct: 11242 atttctcatacttctcgtc 11260

☐ >[gi|15156031|gb|AE008032.1|AE008032](#)  *Agrobacterium tumefaciens* str. C58 circula  
of 254 of the complete sequence  
Length = 10029

Score = 38.2 bits (19), Expect = 2.2  
Identities = 19/19 (100%)  
Strand = Plus / Plus

Query: 47 atttctcatacttctcgtc 65  
|||||  
Sbjct: 361 atttctcatacttctcgtc 379

☐ >[gi|14193024|gb|AC013718.6|](#)  *Homo sapiens* BAC clone RP11-116I17 from 2, complet  
Length = 177855

Score = 38.2 bits (19), Expect = 2.2  
Identities = 19/19 (100%)  
Strand = Plus / Minus

Query: 55 tacttctcgtcaggcgtgg 73  
|||||  
Sbjct: 44290 tacttctcgtcaggcgtgg 44272

☐ >[gi|19909496|gb|AC098742.4|](#) ☒ Mus musculus BAC clone RP23-122N2 from 14, complet  
Length = 218683

Score = 36.2 bits (18), Expect = 8.8  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 42     cttgtatttctcatactt 59  
             |||||  
Sbjct: 93912 cttgtatttctcatactt 93929

☐ >[gi|33147141|gb|AC144644.3|](#) ☒ Medicago truncatula clone mth2-1413, complete sequ  
Length = 117645

Score = 36.2 bits (18), Expect = 8.8  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 11     tcagggttttcggttatcgg 28  
             |||||  
Sbjct: 56388 tcagggttttcggttatcgg 56405

☐ >[gi|18642908|gb|AC080132.6|](#) ☒ Homo sapiens BAC clone RP11-166B20 from 4, complet  
Length = 114320

Score = 36.2 bits (18), Expect = 8.8  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 44     tgtatttctcatacttct 61  
             |||||  
Sbjct: 100043 tgtatttctcatacttct 100026

☐ >[gi|29243387|dbj|AP001011.6|](#) ☒ Homo sapiens genomic DNA, chromosome 18 clone:RP1  
sequence  
Length = 204777

Score = 36.2 bits (18), Expect = 8.8  
Identities = 21/22 (95%)  
Strand = Plus / Plus

Query: 41     acttgatttctcatacttctc 62  
             |||||  
Sbjct: 27088 acttgatttctcacactctc 27109

☐ >gi|29243373|dbj|AP005061.3| ☒ Homo sapiens genomic DNA, chromosome 18 clone:RP1  
sequence  
Length = 186074

Score = 36.2 bits (18), Expect = 8.8  
Identities = 21/22 (95%)  
Strand = Plus / Plus

Query: 41 acttgtattttctcatacttctc 62  
|||||  
Sbjct: 180147 acttgtattttctcatacctctc 180168

☐ >gi|13810526|dbj|AP000923.5| ☒ Homo sapiens genomic DNA, chromosome 11q, clone:R  
sequences  
Length = 170973

Score = 36.2 bits (18), Expect = 8.8  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 44 tgtattttctcatacttct 61  
|||||  
Sbjct: 91047 tgtattttctcatacttct 91064

☐ >gi|15787722|emb|AL162574.14| ☒ Human DNA sequence from clone RP11-282A11 on chr  
sequence  
Length = 184738

Score = 36.2 bits (18), Expect = 8.8  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 3 agagatgttcaggttttc 20  
|||||  
Sbjct: 57310 agagatgttcaggttttc 57293

☐ >gi|16944202|emb|AL603792.12| ☒ Mouse DNA sequence from clone RP23-328B4 on chro  
sequence  
Length = 203030

Score = 36.2 bits (18), Expect = 8.8  
Identities = 18/18 (100%)  
Strand = Plus / Plus

Query: 40 aacttgtattttctcatcac 57  
|||||  
Sbjct: 25030 aacttgtattttctcatcac 25047



☐ >[gi|15128594|dbj|AB055625.1](#) ☒ *Inversidens japonensis* mitochondrial DNA, ND5 to  
haplotype:female type  
Length = 16826

Score = 36.2 bits (18), Expect = 8.8  
Identities = 18/18 (100%)  
Strand = Plus / Minus

Query: 42 cttgtattttctcatactt 59  
|||||  
Sbjct: 2522 cttgtattttctcatactt 2505

☐ >[gi|14043054|emb|AL450324.10](#) ☒ Human DNA sequence from clone RP11-307F22 on chr  
sequence  
Length = 101846

Score = 36.2 bits (18), Expect = 8.8  
Identities = 21/22 (95%)  
Strand = Plus / Minus

Query: 40 aacttgattttctcatacttct 61  
|||||  
Sbjct: 13663 aacttttattttctcatacttct 13642